

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,923

DATE: 10/26/2001

TIME: 14:59:28

Input Set : A:\ES.txt

Output Set: N:\CRF3\10262001\I787923.raw

3 <110> APPLICANT: SANSON, ALAIN
4 RUSSO-MARIE, FRANCOISE
5 NEUMANN, JEAN-MICHEL
6 CORDIER-OCHSENBEIN, FRANCOISE
7 GUEROIS, RAPHAEL
9 <120> TITLE OF INVENTION: CHEMICAL STRUCTURE HAVING AN AFFINITY FOR A PHOSPHOLIPID AND LABELLING
10 COMPOUND, DIAGNOSIS KIT, AND DRUG COMPRISING THIS STRUCTURE
12 <130> FILE REFERENCE: 205399US-0-XPCT
14 <140> CURRENT APPLICATION NUMBER: US 09/787,923
15 <141> CURRENT FILING DATE: 2001-04-02
17 <150> PRIOR APPLICATION NUMBER: FR 98/12366
18 <151> PRIOR FILING DATE: 1998-10-02
20 <150> PRIOR APPLICATION NUMBER: PCT/FR99/02329
21 <151> PRIOR FILING DATE: 1999-09-30
23 <160> NUMBER OF SEQ ID NOS: 5
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 346
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
32 <400> SEQUENCE: 1
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39 20 25 30
42 Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
43 35 40 45
46 Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
47 50 55 60
50 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
51 65 70 75 80
54 Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu
55 85 90 95
58 Lys Lys Ala Leu Thr Gly His Leu Glu Val Val Leu Ala Leu Leu
59 100 105 110
62 Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys
63 115 120 125
66 Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg
67 130 135 140
70 Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu
71 145 150 155 160
74 Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe
75 165 170 175
78 Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe
79 180 185 190
82 Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu
83 195 200 205

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86 Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile
87      210                      215                      220
90 Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr
91 225                      230                      235                      240
94 Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu
95                      245                      250                      255
98 Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr
99      260                      265                      270
102 Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly
103      275                      280                      285
106 Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser
107      290                      295                      300
110 Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly
111 305                      310                      315                      320
114 Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu
115                      325                      330                      335
118 Lys Ile Leu Val Ala Leu Cys Gly Gly Asn
119      340                      345
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 320
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
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133 Glu Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly
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137 Thr Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr Ser Arg Ser Asn Ala
138      35                      40                      45
141 Gln Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp
142      50                      55                      60
145 Leu Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu
146 65                      70                      75                      80
149 Ile Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu
150      85                      90                      95
153 Lys His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu
154      100                     105                     110
157 Ile Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val
158      115                     120                     125
161 Tyr Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp
162      130                     135                     140
165 Thr Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn
166 145                     150                     155                     160
169 Arg Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala
170      165                     170                     175
173 Gln Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu
174      180                     185                     190
177 Lys Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys
178      195                     200                     205

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181 Val Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr
182      210                      215                      220
185 Ile Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val
186 225                      230                      235                      240
189 Val Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr
190                      245                      250                      255
193 Tyr Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val
194                      260                      265                      270
197 Met Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe
198                      275                      280                      285
201 Arg Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr
202      290                      295                      300
205 Ser Gly Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Glu Asp Asp
206 305                      310                      315                      320
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211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 3
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217 1                      5                      10                      15
220 Asp Phe Ser Pro Ser Val Asp Ala Glu Ala Ile Gln Lys Ala Ile Arg
221                      20                      25                      30
224 Gly Ile Gly Thr Asp Glu Lys Met Leu Ile Ser Ile Leu Thr Glu Arg
225                      35                      40                      45
228 Ser Asn Ala Gln Arg Gln Leu Ile Val Lys Glu Tyr Gln Ala Ala Tyr
229      50                      55                      60
232 Gly Lys Glu Leu Lys Asp Asp Leu Lys Gly Asp Leu Ser Gly His Phe
233 65                      70                      75                      80
236 Glu His Leu Met Val Ala Leu Val Thr Pro Pro Ala Val Phe Asp Ala
237                      85                      90                      95
240 Lys Gln Leu Lys Lys Ser Met Lys Gly Ala Gly Thr Asn Glu Asp Ala
241                      100                     105                     110
244 Leu Ile Glu Ile Leu Thr Thr Arg Thr Ser Arg Gln Met Lys Asp Ile
245                      115                     120                     125
248 Ser Gln Ala Tyr Tyr Thr Val Tyr Lys Lys Ser Leu Gly Asp Asp Ile
249      130                     135                     140
252 Ser Ser Glu Thr Ser Gly Asp Phe Arg Lys Ala Leu Leu Thr Leu Ala
253 145                     150                     155                     160
256 Asp Gly Arg Arg Asp Glu Ser Leu Lys Val Asp Glu His Leu Ala Lys
257                      165                      170                      175
260 Gln Asp Ala Gln Ile Leu Tyr Lys Ala Gly Glu Asn Arg Trp Gly Thr
261                      180                      185                      190
264 Asp Glu Asp Lys Phe Thr Glu Ile Leu Cys Leu Arg Ser Phe Pro Gln
265                      195                      200                      205
268 Leu Lys Leu Thr Phe Asp Glu Tyr Arg Asn Ile Ser Gln Lys Asp Ile
269      210                     215                     220
272 Val Asp Ser Ile Lys Gly Glu Leu Ser Gly His Phe Glu Asp Leu Leu
273 225                     230                     235                     240

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276 Leu Ala Ile Val Asn Cys Val Arg Asn Thr Pro Ala Phe Leu Ala Glu
277           245           250           255
280 Arg Leu His Arg Ala Leu Lys Gly Ile Gly Thr Asp Glu Phe Thr Leu
281           260           265           270
284 Asn Arg Ile Met Val Ser Arg Ser Glu Ile Asp Leu Leu Asp Ile Arg
285           275           280           285
288 Thr Glu Phe Lys Lys His Tyr Gly Tyr Ser Leu Tyr Ser Ala Ile Lys
289           290           295           300
292 Ser Asp Thr Ser Gly Asp Tyr Glu Ile Thr Leu Leu Lys Ile Cys Gly
293 305           310           315           320
296 Gly Asp Asp
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 85
302 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 4
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311 Met Glu Asp Ala Gln Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr
312           20           25           30
315 Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr Arg Asn Thr Ala Gln
316           35           40           45
319 Arg Gln Glu Ile Arg Thr Ala Tyr Lys Ser Thr Ile Gly Arg Asp Leu
320           50           55           60
323 Ile Asp Asp Leu Lys Ser Glu Leu Ser Gly Asn Phe Glu Gln Val Ile
324 65           70           75           80
327 Val Gly Met Met Thr
328           85
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332 <211> LENGTH: 235
333 <212> TYPE: PRT
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336 <400> SEQUENCE: 5
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342 Gly Ala Gly Thr Asp Glu Gly Cys Leu Ile Glu Ile Leu Ala Ser Arg
343           20           25           30
346 Thr Pro Glu Glu Ile Arg Arg Ile Asn Gln Thr Tyr Gln Leu Gln Tyr
347           35           40           45
350 Gly Arg Ser Leu Glu Asp Asp Ile Arg Ser Asp Thr Ser Phe Met Phe
351           50           55           60
354 Gln Arg Val Leu Val Ser Leu Ser Ala Gly Gly Arg Asp Glu Gly Asn
355 65           70           75           80
358 Tyr Leu Asp Asp Ala Leu Val Arg Gln Asp Ala Gln Asp Leu Tyr Glu
359           85           90           95
362 Ala Gly Glu Lys Lys Trp Gly Thr Asp Glu Val Lys Phe Leu Thr Val
363           100          105          110
366 Leu Cys Ser Arg Asn Arg Asn His Leu Leu His Val Phe Asp Glu Tyr
367           115          120          125

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370 Lys Arg Ile Ser Gln Lys Asp Ile Glu Gln Ser Ile Lys Ser Glu Thr
371      130      135      140
374 Ser Gly Ser Phe Glu Asp Ala Leu Leu Ala Ile Val Lys Cys Met Arg
375 145      150      155      160
378 Asn Lys Ser Ala Tyr Phe Ala Glu Lys Leu Tyr Lys Ser Met Lys Gly
379      165      170      175
382 Leu Gly Thr Asp Asp Asn Thr Leu Ile Arg Val Met Val Ser Arg Ala
383      180      185      190
386 Glu Ile Asp Met Leu Asp Ile Arg Ala His Phe Lys Arg Leu Tyr Gly
387      195      200      205
390 Lys Ser Leu Tyr Ser Phe Ile Lys Gly Asp Thr Ser Gly Asp Tyr Arg
391      210      215      220
394 Lys Val Leu Leu Val Leu Cys Gly Gly Asp Asp
395 225      230      235

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VERIFICATION SUMMARY

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